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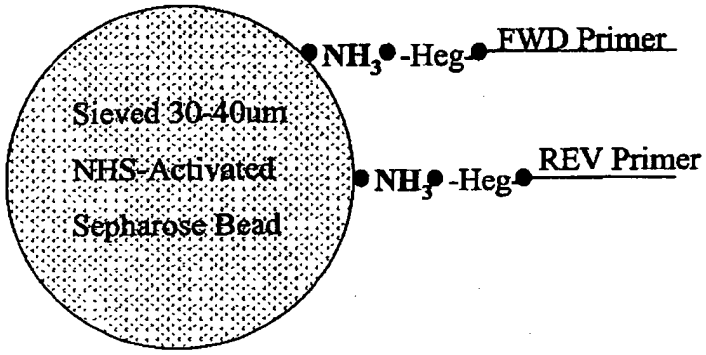
FIGURE 1

A

Sieved 30-40um
NHS-Activated
Sepharose Bead

B


NH3 -Heg FWD Primer
Sieved 30-40um
NHS-Activated
Sepharose Bead
NH3 -Heg REV Primer

C

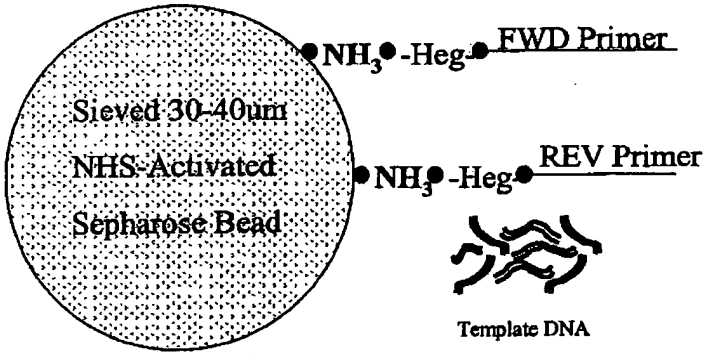
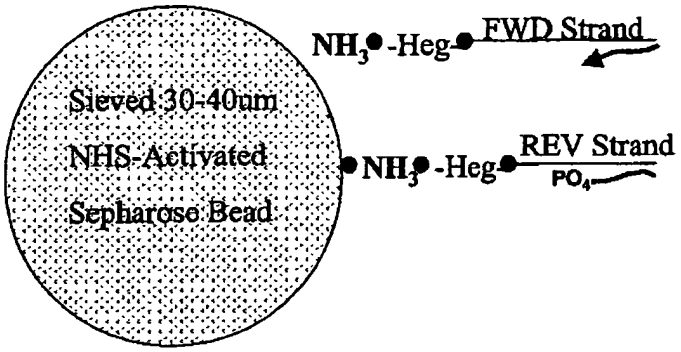
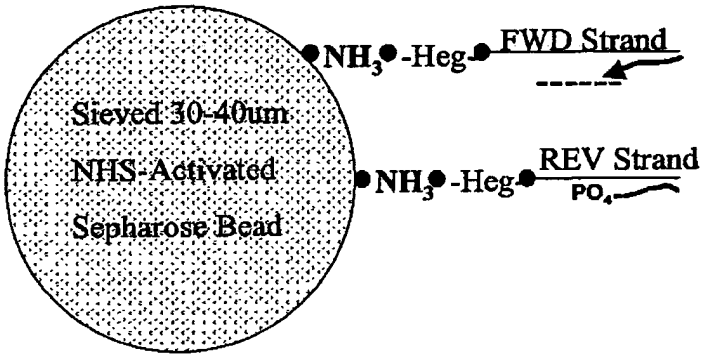

NH3 -Heg FWD Primer
Sieved 30-40um
NHS-Activated
Sepharose Bead
NH3 -Heg REV Primer
Template DNA

FIGURE 1

D


NH3-Heg-FWD Strand
Sieved 30-40um
NHS-Activated
Sepharose Bead
NH3-Heg-REV Strand
PO4

E


NH3-Heg-FWD Strand
Sieved 30-40um
NHS-Activated
Sepharose Bead
NH3-Heg-REV Strand
PO4

F

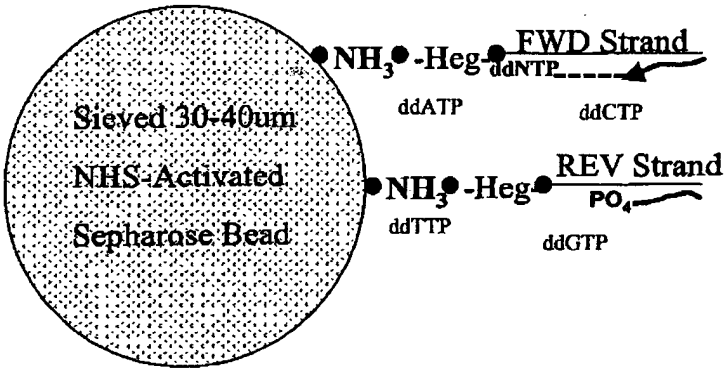
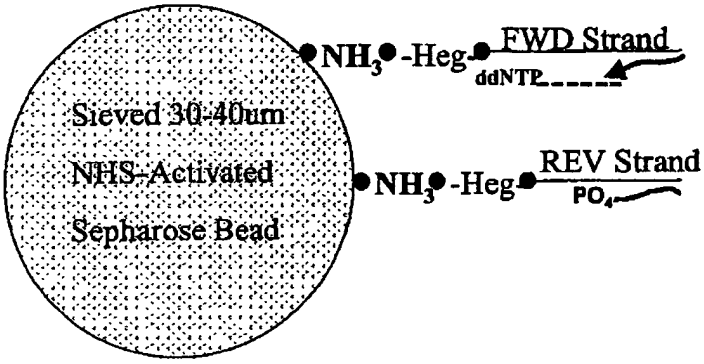
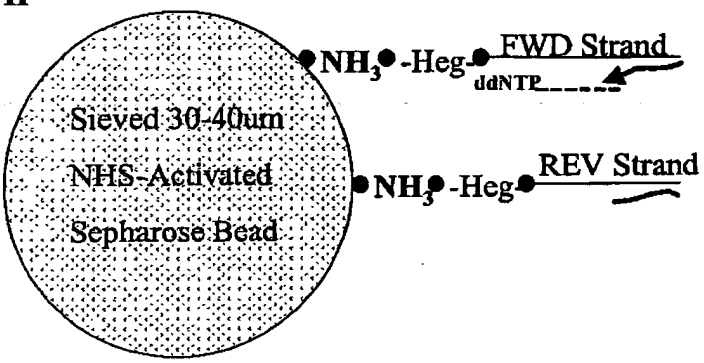

NH3-Heg-FWD Strand
ddNTP
ddATP
ddCTP
Sieved 30-40um
NHS-Activated
Sepharose Bead
NH3-Heg-REV Strand
PO4
ddTTP
ddGTP

FIGURE 1

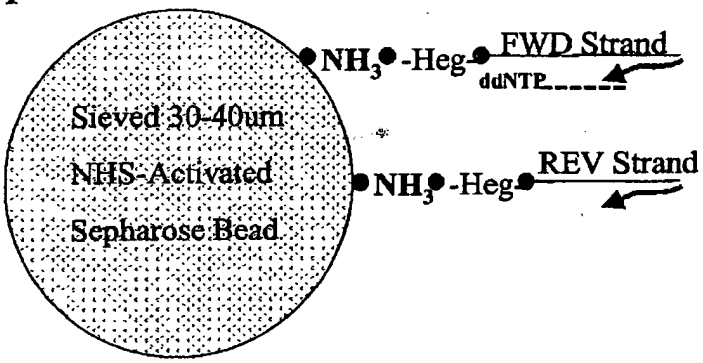
G



H



I



J

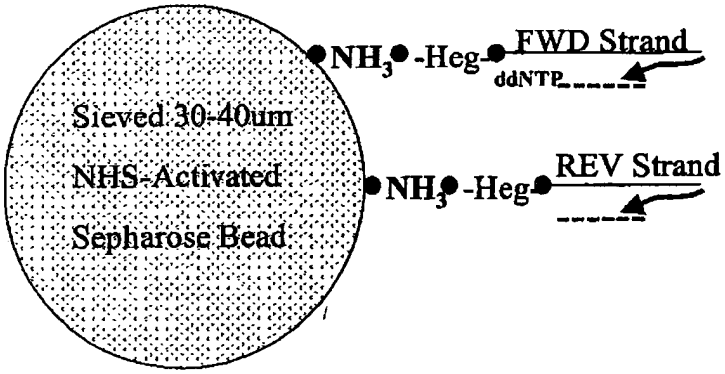


FIGURE 2

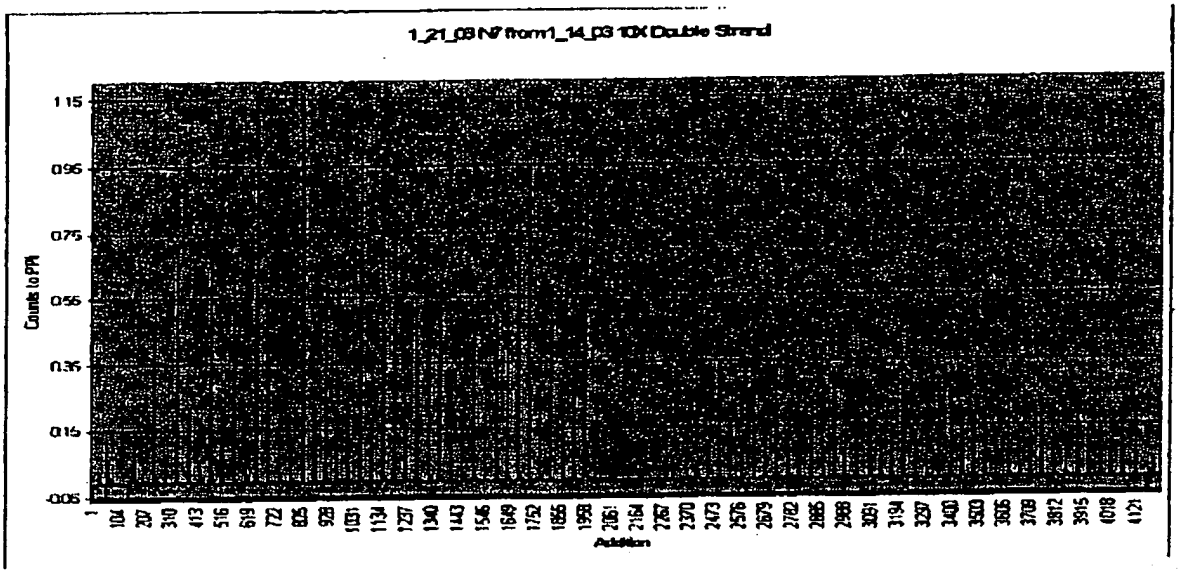
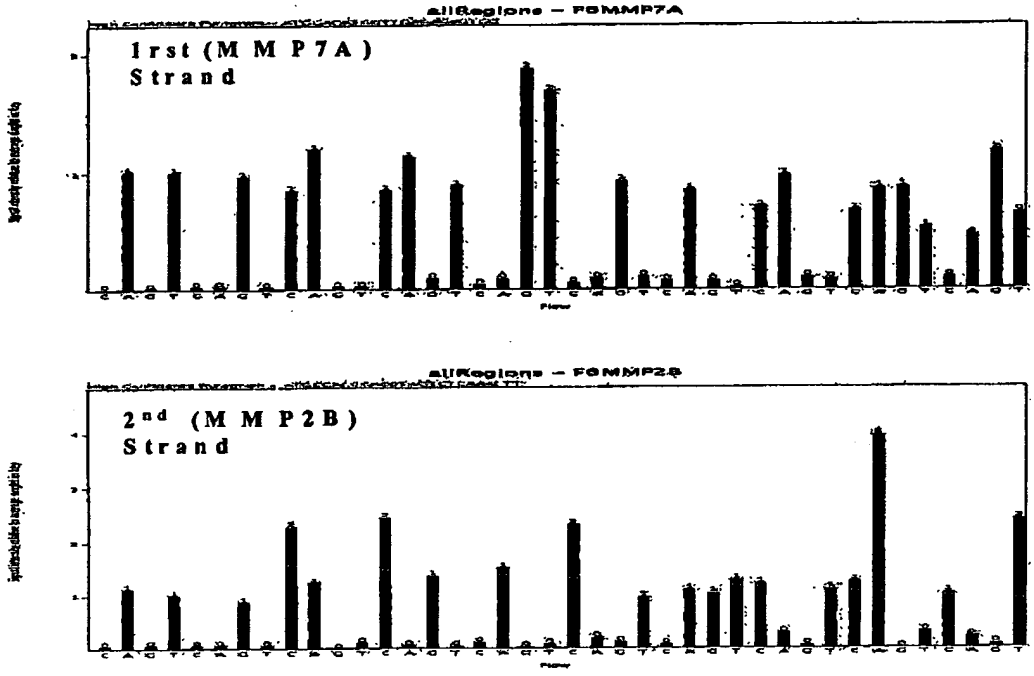

1_21_03 N7 from1_14_03 10X Double Strand
Counts to PPI
1.15
0.95
0.75
0.55
0.35
0.15
-0.05
Addition

FIGURE 3

A)



1rst Strand (MMP7A)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00001_1362_1660.well	ATGCACATGGTTGACACAGTGGT	22

ATGC ACATGGTTGACACAGTGG

ATGC CACCGACCTAGTCTCAAACTT

2nd Strand (MMP2B)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003_1363_1660.well	ATGCCACCGACCTAGTCTCAAACTT	25

FIGURE 4

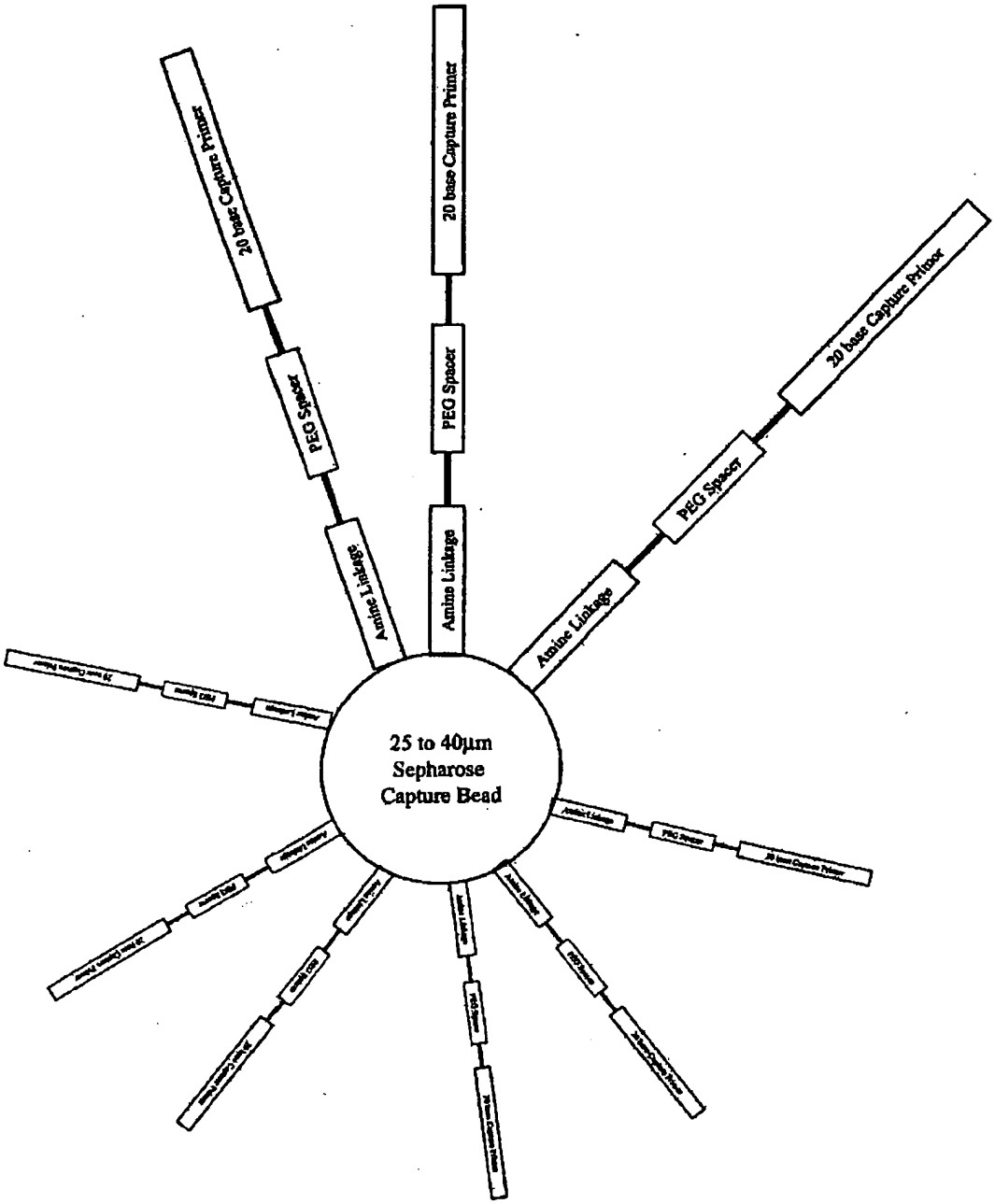

20 base Capture Primer
PEG Spacer
Amine Linkage
20 base Capture Primer
PEG Spacer
Amine Linkage
20 base Capture Primer
PEG Spacer
Amine Linkage
25 to 40µm
Sepharose
Capture Bead

Fig. 5

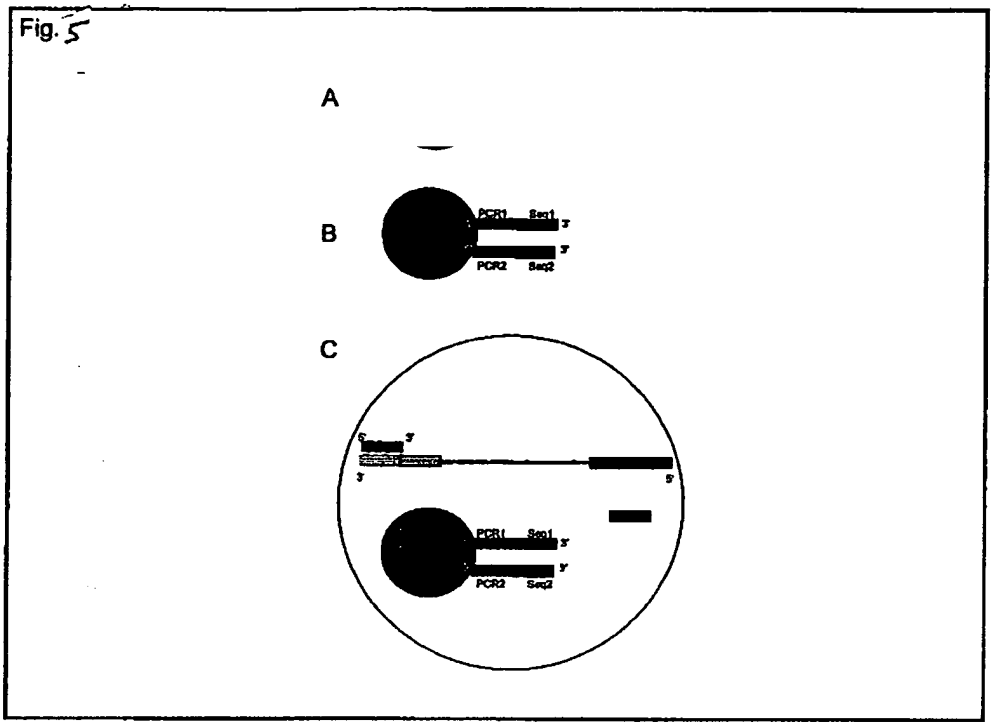

A
B
PCR1
Seq1
3'
3'
PCR2
Seq2
C
5'
3'
3'
5'
PCR1
Seq1
3'
3'
PCR2
Seq2

Fig. 6

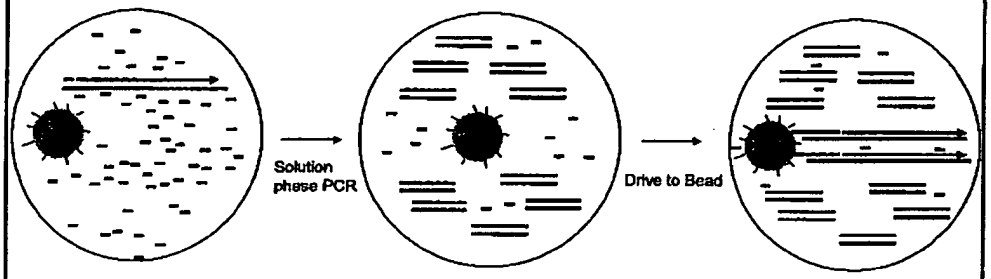

Solution
phase PCR
Drive to Bead

Fig. 7

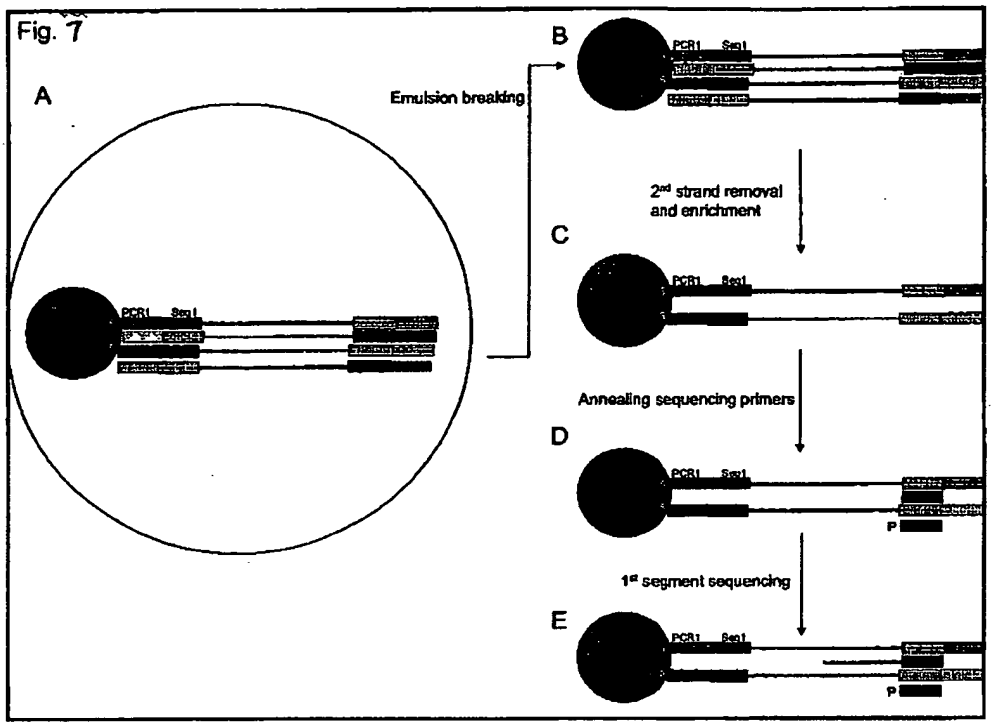

A
Emulsion breaking
B
PCR1
Seq1
2nd strand removal and enrichment
C
Annealing sequencing primers
D
P
1st segment sequencing
E

Fig. 8

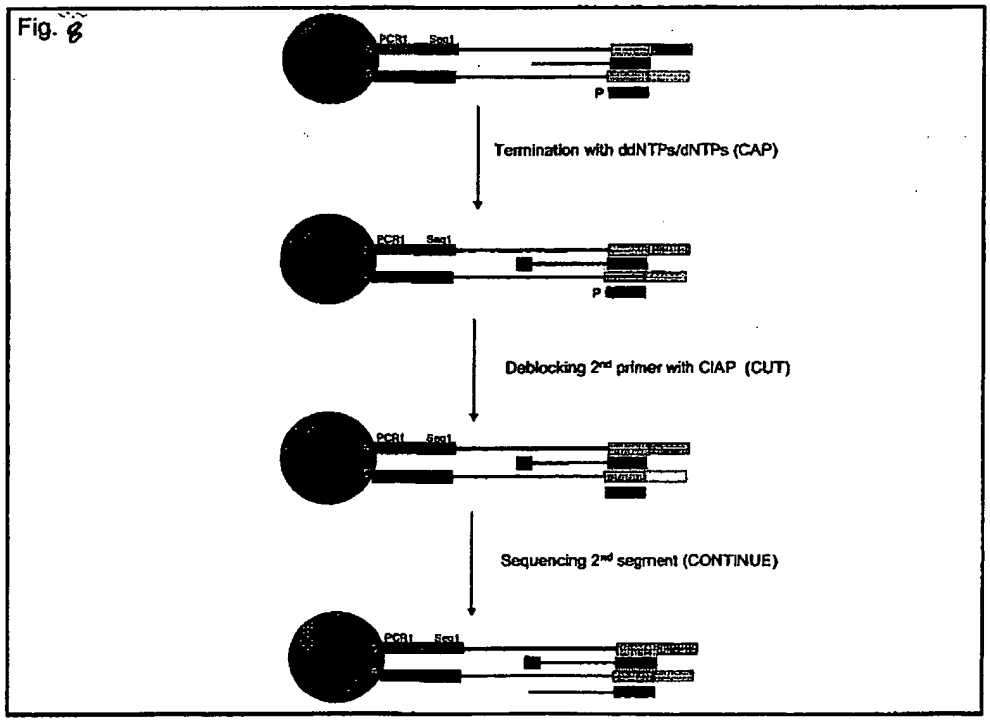
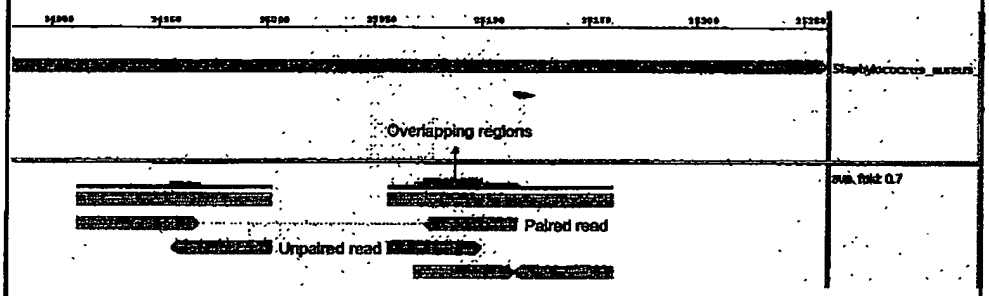

PCR1
Seq1
P
Termination with ddNTPs/dNTPs (CAP)
Deblocking 2nd primer with CIAP (CUT)
Sequencing 2nd segment (CONTINUE)

Fig. 9

A



B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

Fig. 10

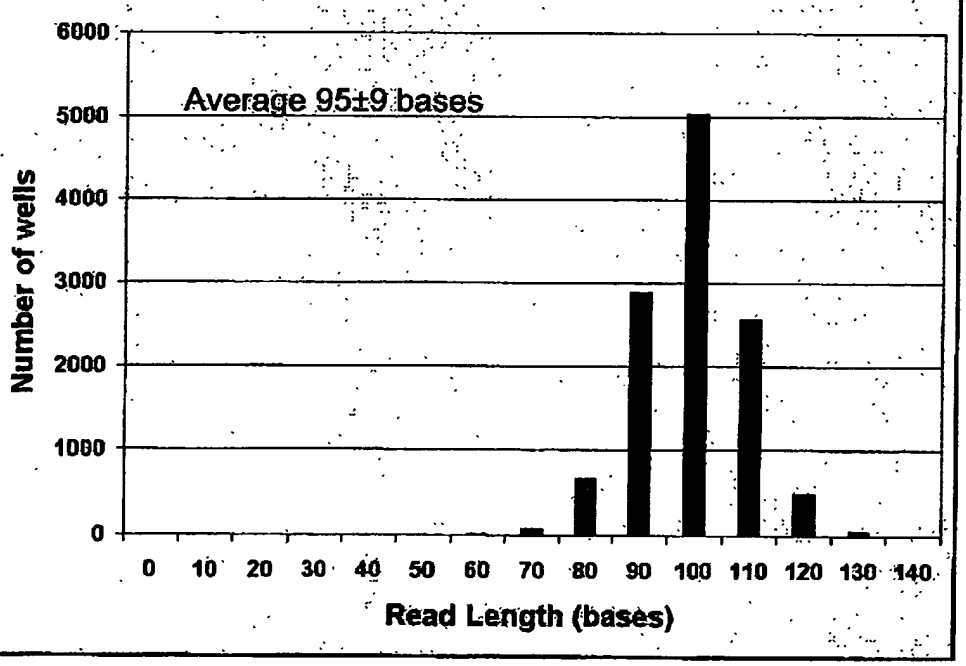


Fig. 11

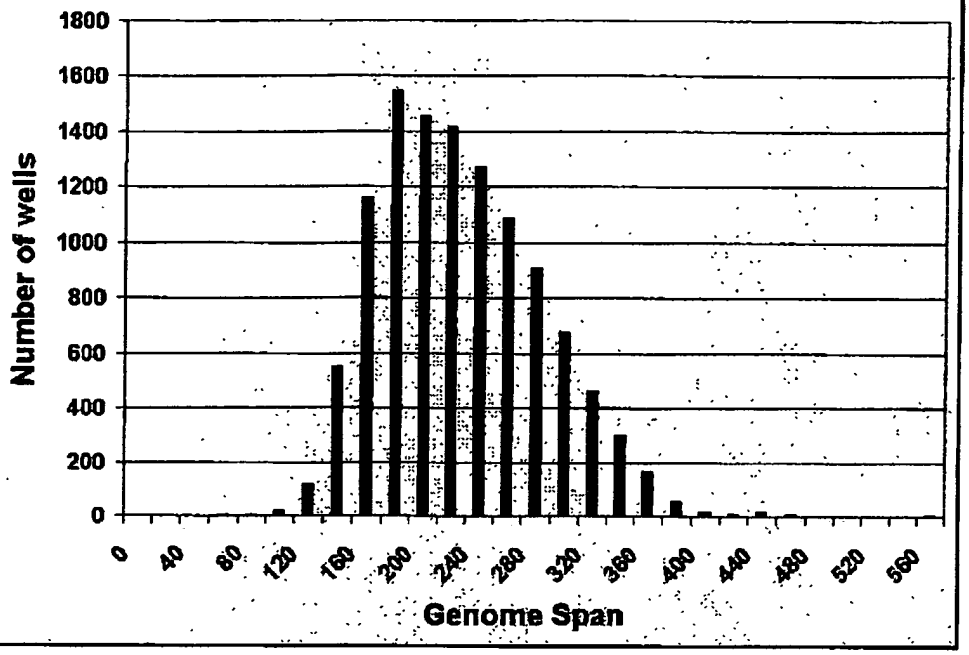


Fig. 12

Well	Genome Position	Orientation	Alignment String
00364_0548_2609	571366	F	TATTGTTGATGCTGTAAAAaGAAGCTACTGGTGTAGtATTTTTATGAAGTT
00364_0548_2609_D2	571512	R	TGCTCAAAGAATTCATTTAAAATATGACCATATTTCATTGTATCTTT
00383_0985_2232	1487690	R	AAGCGAACAGTCAAGTACCACAGTCAGTTGACTTTACACAAGCGGAT
00383_0985_2232_D2	1487769	F	TACAGGTGTTGGTATGCCATTTGCGATTTGTTGCGCTTGGTTAGCCG
00397_0940_2923	2611033	F	AACATATAAACATCCCCTATCTCAATTTCCGCTTCCATGTAaCAAAAAAAGC
00397_0940_2923_D2	2611164	R	TAGATATCACTTGCGTGTTACTGGTAATGCAGGCATGAG
00417_0611_1933	122001	R	ATTCAACTCTGGAAATGCtTTCTTGATACGCCTCGATGATG
00417_0611_1933_D2	121930	F	GATGAGGAGCTGCAATGGCAATGGGTTAAAGGCATCATCG
00434_0595_0993	2022591	R	TGTATCTCGATTTGGATTAGTTGCTTTTGCATCTTCATTAGACC
00434_0595_0993_D2	2022473	F	CATTAACATCTGCACCAGAAATAGCTTCTAATACGATTGC
00443_1003_0754	107373	F	GCGACGACGTCCAGCTAATAACGCTGCACCTAAGGCTAATGATAAT
00443_1003_0754_D2	107502	R	AAACCATGCAGATGCTAACAAAGCTCAAGCATTACCAGAAACT
00454_1257_3047	59036	R	TGTTGCTGCATCATAATTTAATACTACATCATTTAAtTCTTTGG
00454_1257_3047_D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT